【Sequence Listing】

<110>   Lifenza Co., Ltd.

<120>   PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH, MUTAN,
         INULIN AND LEVANN, GENE ENCODING THE SAME, CELL EXPRESSING THE
         SAME, AND PRODUCTION METHOD THEREOF

<150>   KR2004-0006185
<151>   2004-01-30

<160>   4

<170>   KopatentIn 1.71

<210>   1
<211>   608
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   S. cerevisiae/pYES2-LSD1

<400>   1
Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile
 1   5   10   15

Thr Arg Ile Val Leu Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly
             20   25   30

Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu
             35   40   45

Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val
    50   55   60

Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser

Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile
　　　　　　　　　85　　　　　　　　90　　　　　　　　95

5

Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn
　　　　　　　100　　　　　　　105　　　　　　　110

Ser Asn_Thr Leu Asn Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro
10　　　　　115　　　　　　　120　　　　　　　125

Ser Leu Gly Ile Asn Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp
　　　　130　　　　　　　135　　　　　　　140

15 Val Asp Ile Lys Ile Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro
　145　　　　　　　150　　　　　　　155　　　　　　　160

Leu Asp Ile Val Ile Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg
　　　　　　　165　　　　　　　170　　　　　　　175

20

Cys Val Gly Gly Ile Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg
　　　　　　　180　　　　　　　185　　　　　　　190

Lys Phe Ser Val Glu Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp
25　　　　　195　　　　　　　200　　　　　　　205

Gly Ser Gln Tyr Val Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro
　　　　　210　　　　　　　215　　　　　　　220

30 Lys Asn Ala Leu Val Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met
　225　　　　　　　230　　　　　　　235　　　　　　　240

Val Pro His Met Thr Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro
　　　　　　　245　　　　　　　250　　　　　　　255

35

Ile Asn Asn Gly Asp Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro
　　　　　260　　　　　　　265　　　　　　　270

```
        Gly Val Tyr Trp Met Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu
                275                 280                 285
```

5
```
        Gly Ser Asn His Met Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu
                290                 295                 300
```

```
        Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln
        305             310                 315                 320
```
10
```
        Asn Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val
                        325                 330                 335
```

```
        Tyr Gln Ala Asn Ala Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly
15                      340                 345                 350
```

```
        Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr
                    355                 360                 365
```

20
```
        Trp Phe Cys Met Gly Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met
                370                 375                 380
```

```
        Asp Phe Asn Gly Asn Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys
        385                 390                 395                 400
```
25
```
        Gln Val Gly Ala Tyr Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu
                        405                 410                 415
```

```
        Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile
                    420                 425                 430
```
30
```
        Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys
                    435                 440                 445
```

35
```
        Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu
                450                 455                 460
```

Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe
465   470   475   480

Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe
                485   490   495

Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr
             500   505   510

Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile
             515   520   525

Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe
    530   535   540

Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile
545   550   555   560

Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr
             565   570   575

Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu
             580   585   590

Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
             595   600   605

<210>   2
<211>   2052
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   S. cerevisiae/pYLSD1

<400>   2

    tgggtgtgtc ccttgctctg ccaacgttgt tgattgtttt catgacatta atctacgtgc   60

    cttcaatatt tacaatggtc ccctcaatca cacggattgt actggttaac attctgttgg   120

    cgacgttggt tttgggagct gcagtccttc cacgagacaa cagaactgtt tgcgggagtc   180

    aactctgcac atggtggcac gactccggcg agataaacac cggtactcct gtacaggcag   240

    gaaacgttcg acaatcccga aagtactctg tccatgtgag cctggcagac cgtaaccaat   300

    tctacgactc tttcgtatat gaatcgatac ctaggaacgg caatggcaga atttattctc   360

    ccaccgaccc acctaacagc aatacattga atagtagcat tgacgacggt atatcaatcg   420

    aaccatctct cggcatcaac atggcttggt cccagttcga atatagacga gatgtcgaca   480

    ttaagattac tacaatcgat ggctcaatat tggatggccc tttggacatt gttattcggc   540

    cgacttctgt taagtactca gtcaaaagat gtgtgggtgg tatcattatt agagtccctt   600

    atgatcccaa tggtcgaaaa ttctctgttg agttaaagag tgacctttac agttacctct   660

    ccgacggttc gcaatatgtg acctctggag ggagcgtggt tggtgtggag ccaaaaaatg   720

    ccctggtgat ctttgccagc cctttcttgc cacgggatat ggttcctcat atgacaccac   780

    acgacaccca gacaatgaag ccgggcccaa tcaataatgg ggactggggt tcaaagccta   840

    tactctactt cccgcctggc gtatactgga tgaacgagga tacctctggt aaccccggga   900

    agctcggctc aaatcatatg cggctggatc ccaataccta ctgggtccat ctagccccag   960

    gagcctatgt gaaaggagcc attgagtatt tcacgaagca aaatttctat gcaacgggtc   1020

```
     atggcgttct ctcaggtgag aactatgttt atcaggccaa tgcagctgat aactactatg      1080

     ccgtcaagag tgatggcaca agcttgagaa tgtggtggca caacaacctt ggaggcggtc      1140

5    aaacatggtt ttgcatgggg cccaccatta atgcaccgcc gtttaatacg atggacttca      1200

     acggaaactc taatatttcc agccggatta gtgactataa gcaggttggc gcttattttt      1260

     tccaaacaga cggaccggag atctacgagg acagtgttgt ccatgacgtc ttctggcatg      1320
10
     ttaatgatga tgccatcaag acatattatt ccggagcttc aatttcacga gcaaccatct      1380

     ggaagtgtca caatgacccg atcatacaga tgggctggac gtcacgaaat ctcaccggaa      1440

15   tcagcattga taacctgcac gtcatccaca cgagatattt caaatctgaa acagtggttc      1500

     cttcagcaat cattggagcg tctccattct acgcaagtgg aatgactgtt gatcccagcg      1560

     agtccatcag catgaccatc tctaacgtgg tgtgtgaggg tctatgcccc tcactgttcc      1620
20
     gtatcactcc gcttcagagc tacaacaacc ttgttgtcaa gaacgtggcc tttcccgatg      1680

     gactgcagac aaatccaatc ggaataggag agagcattat accagcagct tccggctgta      1740

25   caatggactt ggaaatcaca aactggaccg tcaaaggaca aaaagtcacc atgcaaaact      1800

     ttcagtccgg gtcacttggc cagttcgata tcgatggttc atactggggt caatggtcca      1860

     taaactaaag ctattcccat tcacctgagt attttcgtgg gttcaatgag ttcttgttac      1920
30
     tgatggggcc cttgctagtg gtaaaagtag agggacttgt cctcgccggg cgccaaggaa      1980

     gttcatgtct tctagttgaa tagtatttgt ttcttctctc tcgttaaaaa aaaaaaaaaa      2040

35   aaaaaaaaaa aa                                                           2052
```

```
<210>    3
<211>    18
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    L. starkeyi DX-F primer(sense)


<400>    3
gtcccttgag ctcccaac                                                    18



<210>    4
<211>    23
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    L. starkeyi DX-R primer(antisense)


<400>    4
tcaactagaa ttcatgaact tcc                                              23
```